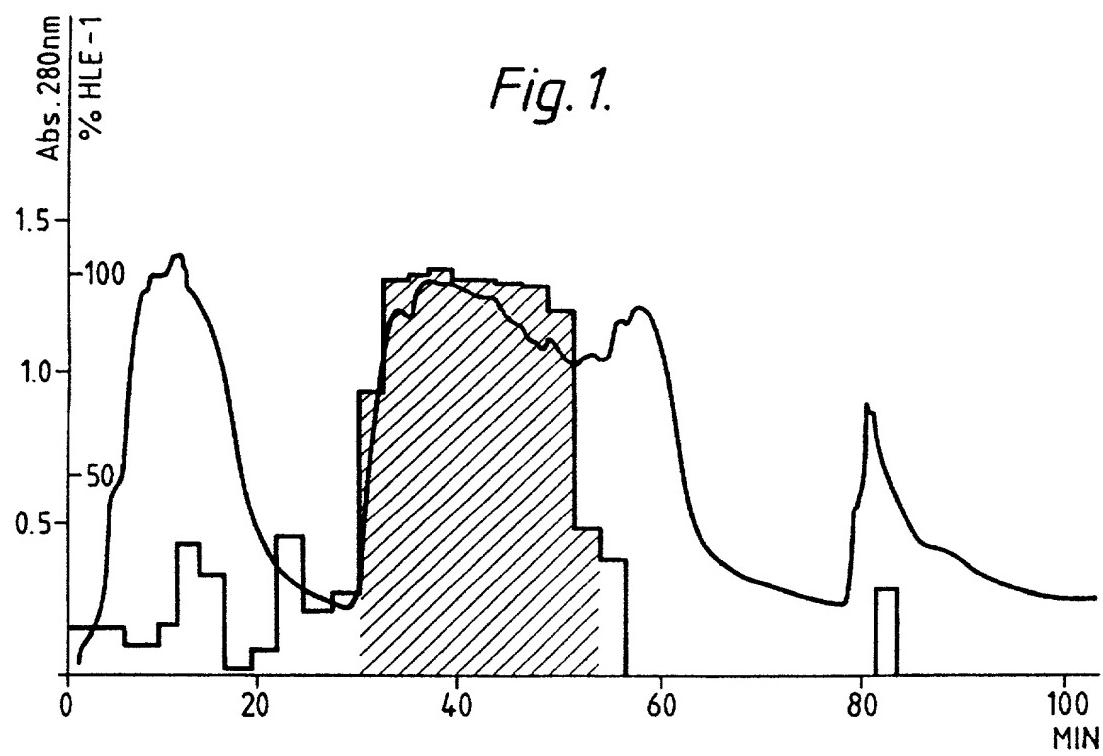
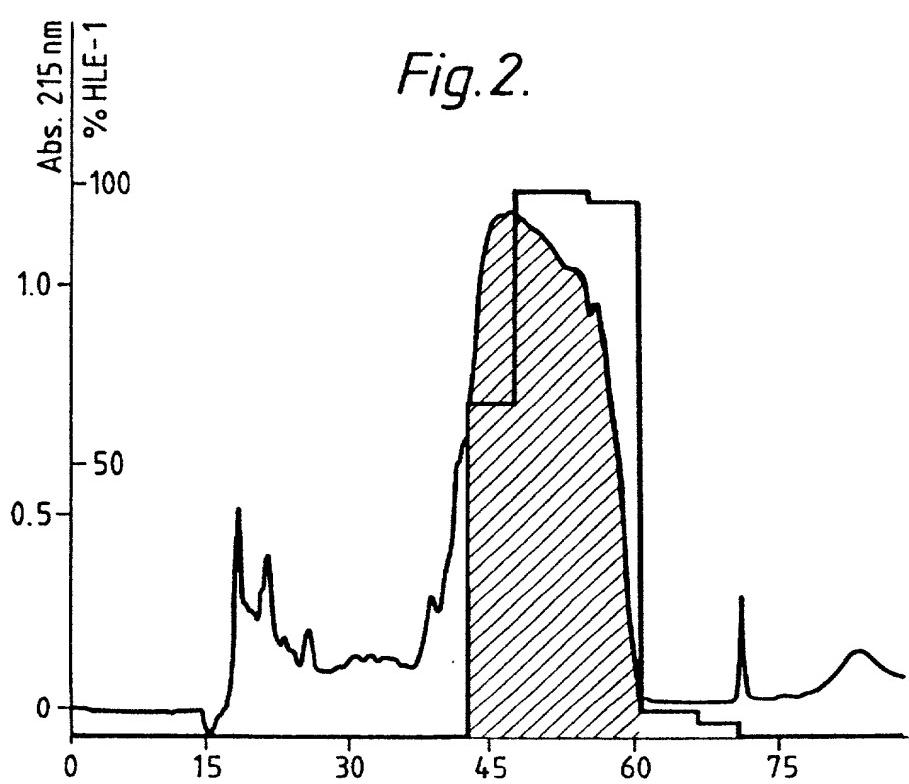


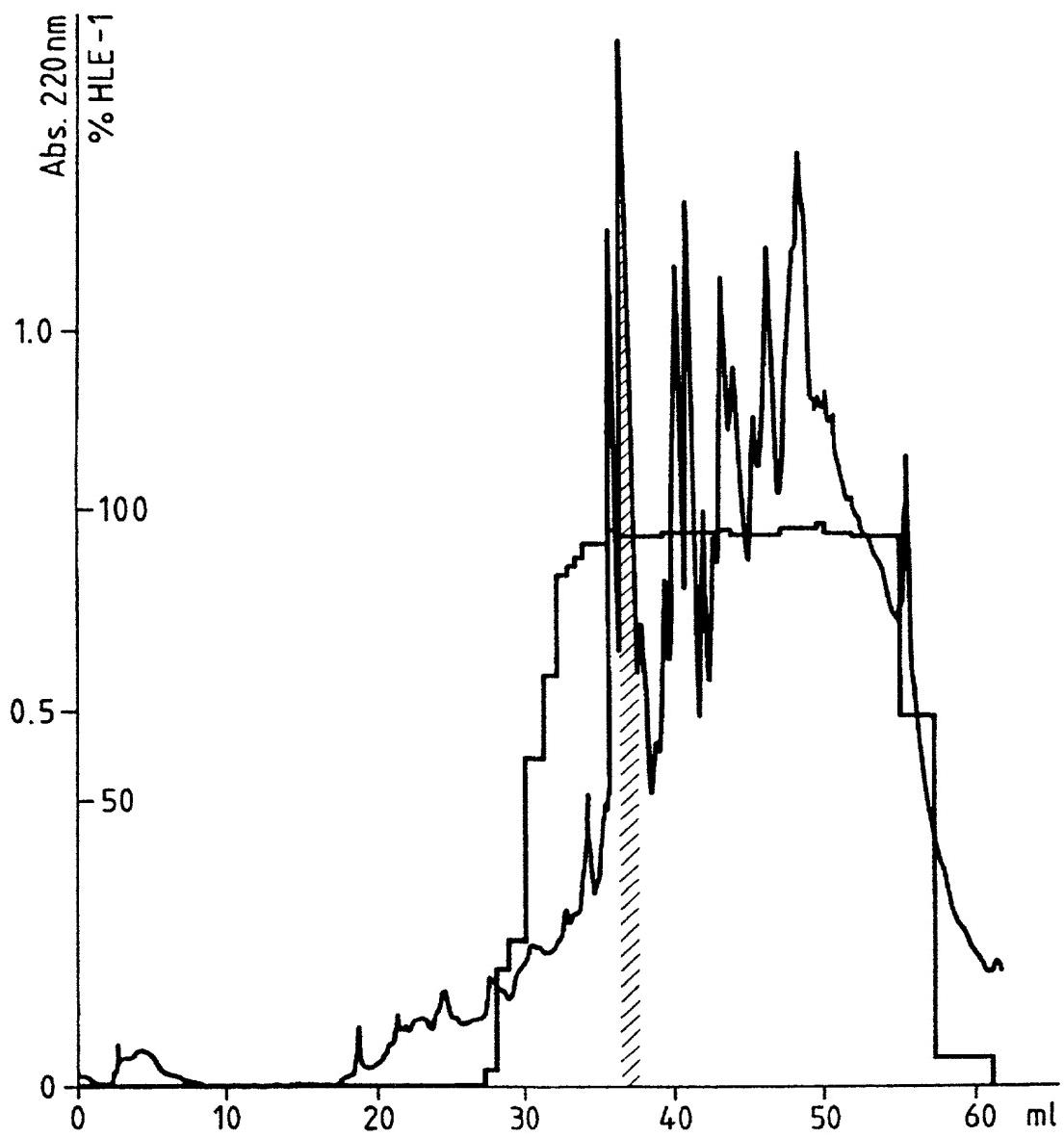
*Fig. 1.*



*Fig. 2.*

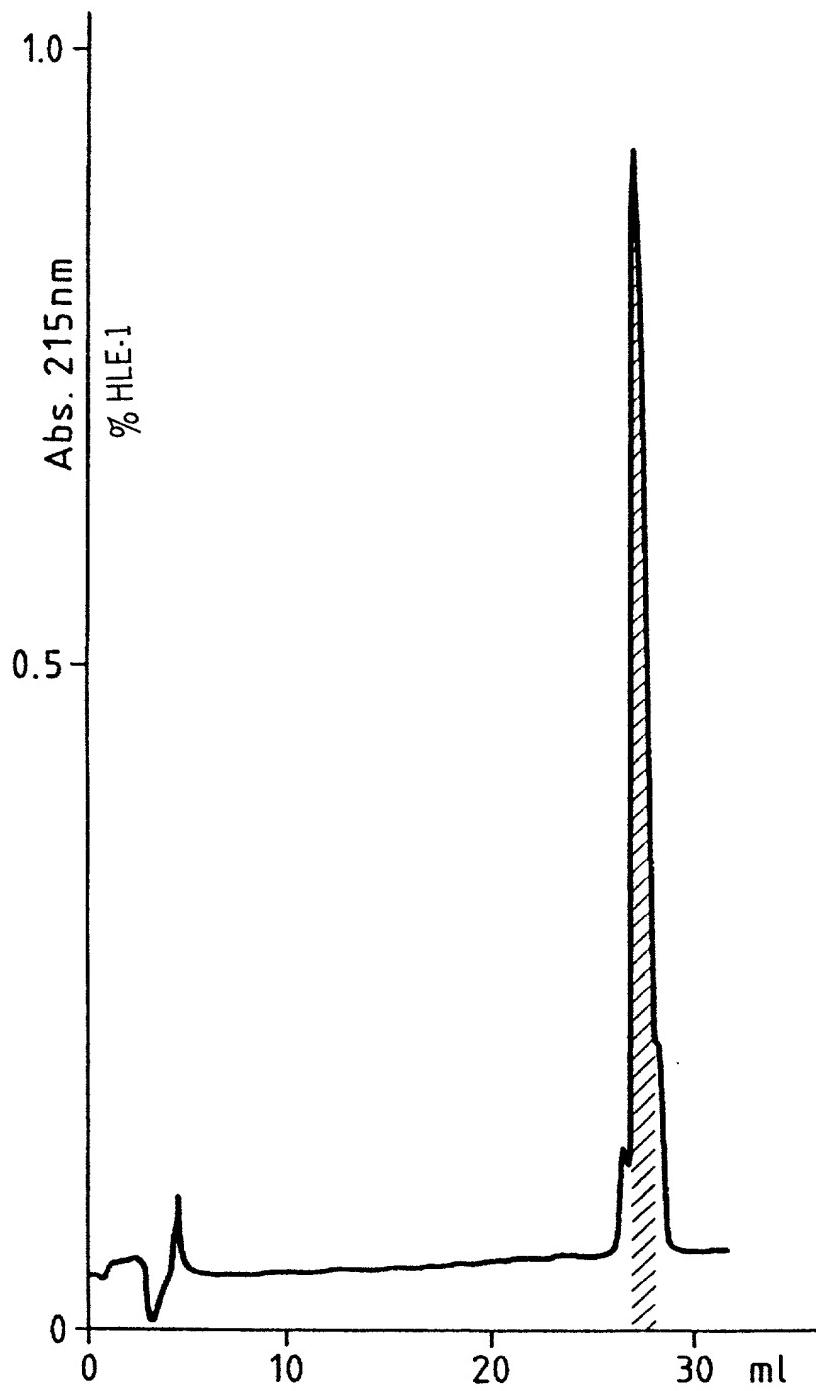


*Fig. 3.*



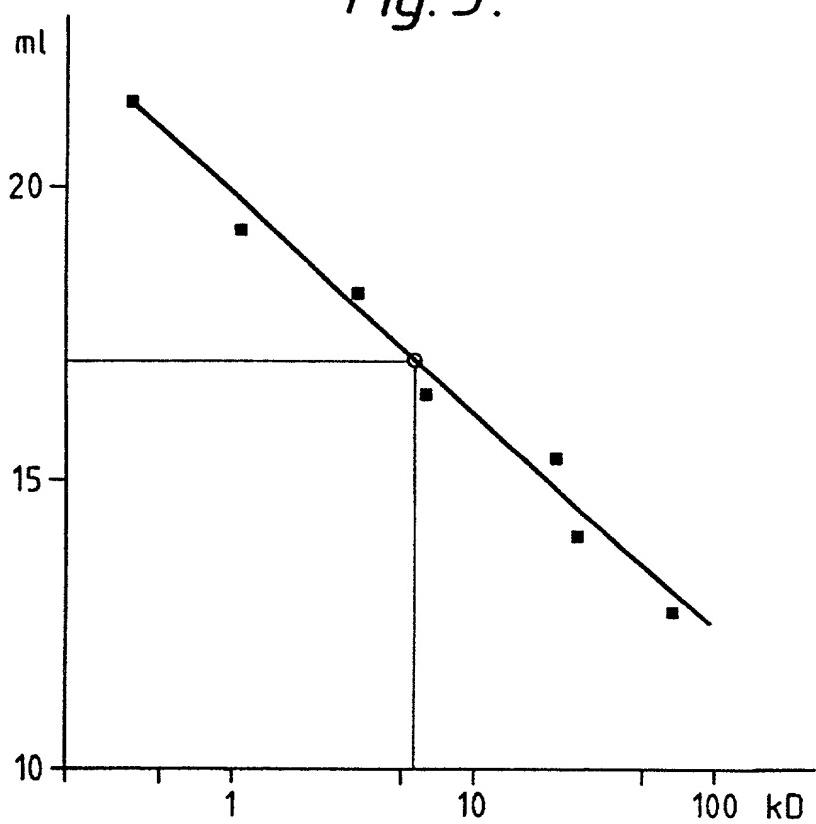
*Fig. 4.*

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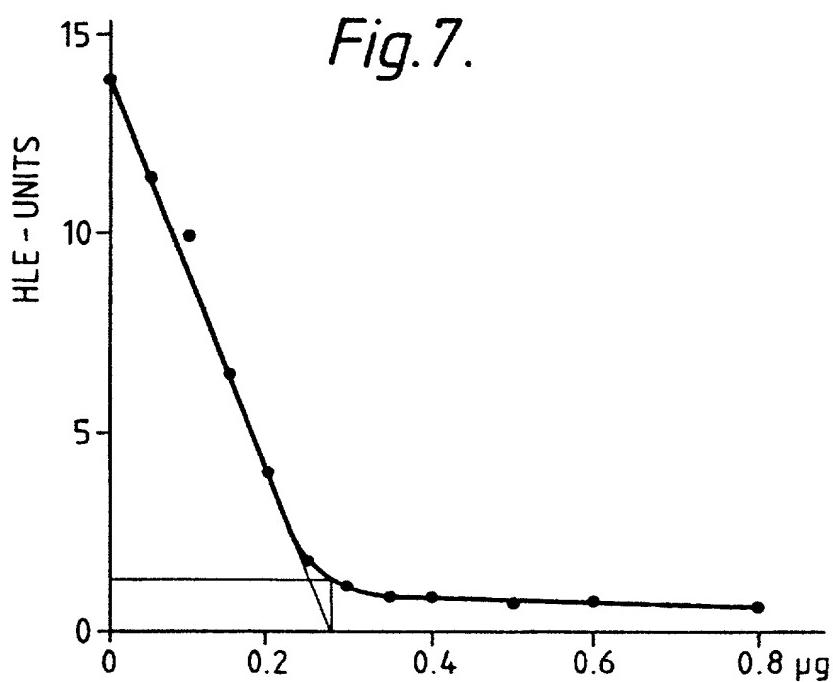


*Fig. 5.*

bioassay of  $\text{H}_2\text{O}_2$  by  $\text{H}_2\text{O}_2$  - catalase system



*Fig. 7.*



*Fig. 6.*

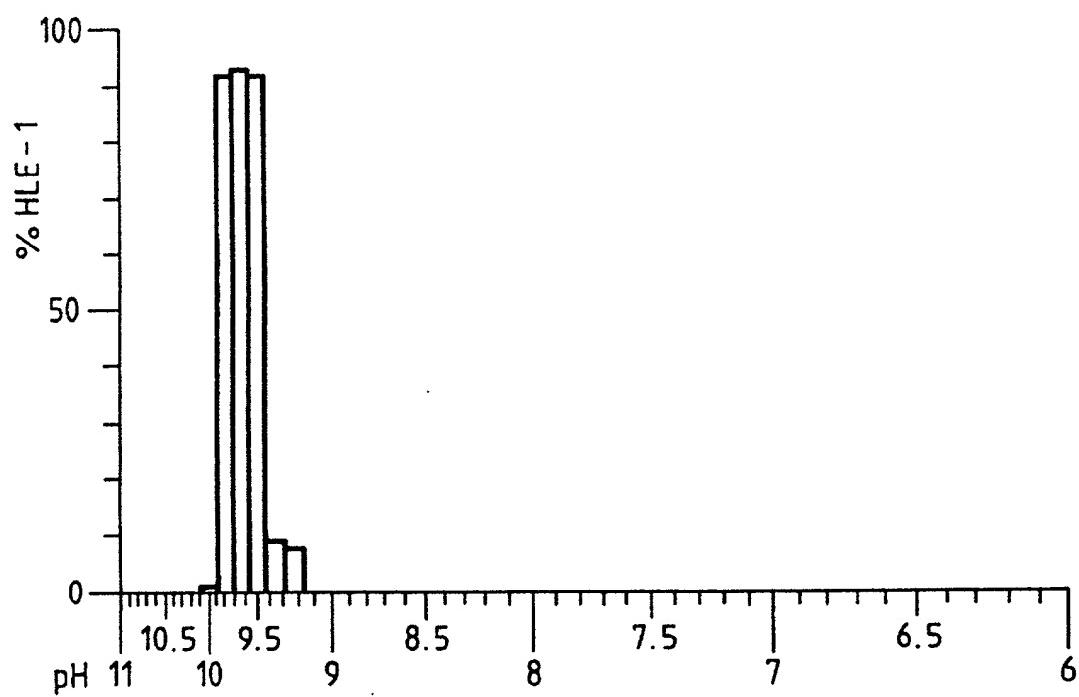
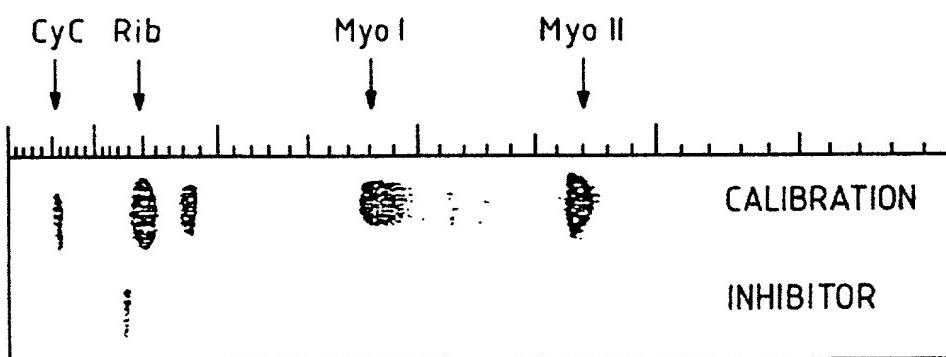


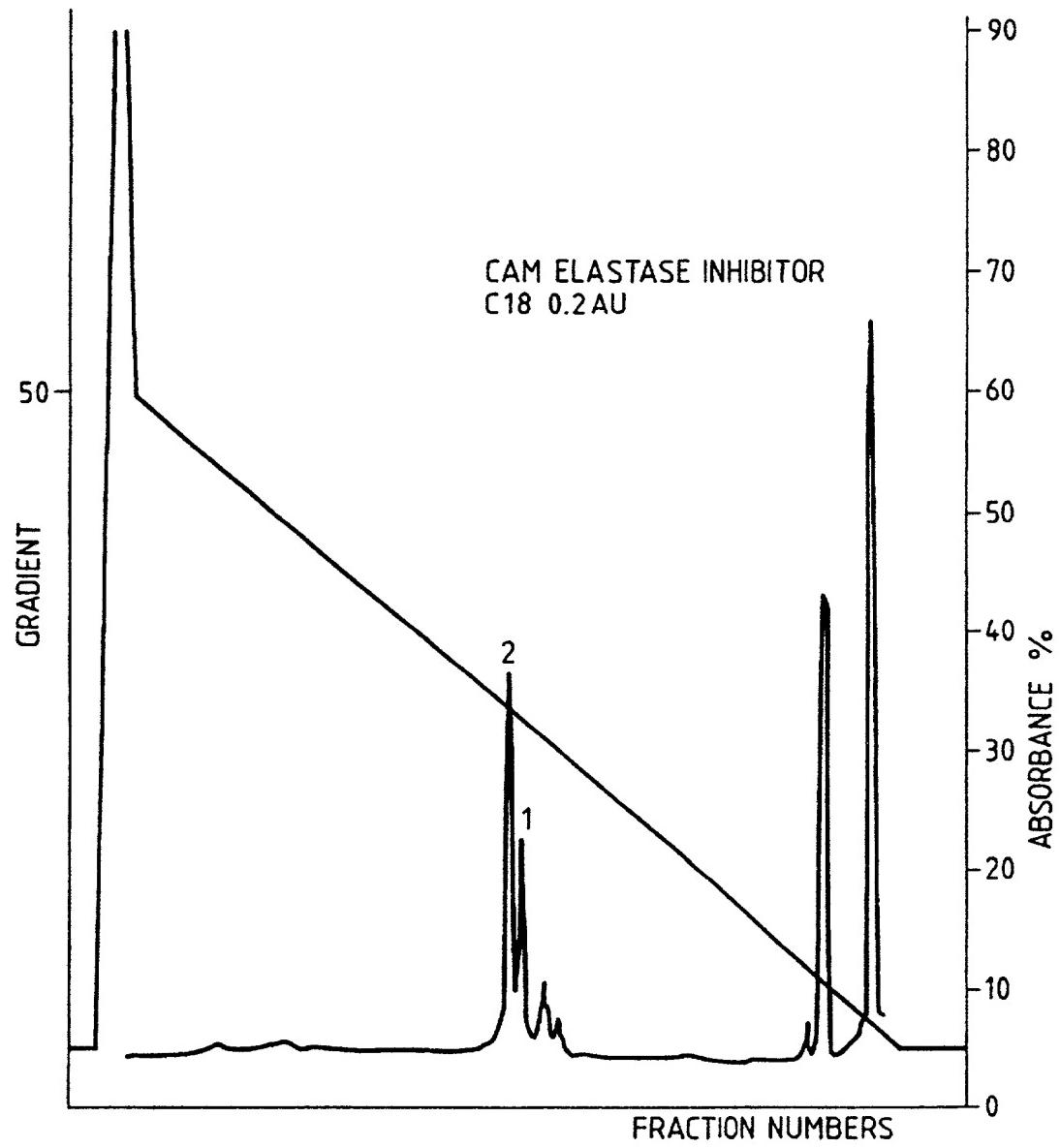
Fig. 8.

## PROTEIN SEQUENCE OF ELASTASE INHIBITOR

DIRECT SEQUENCE

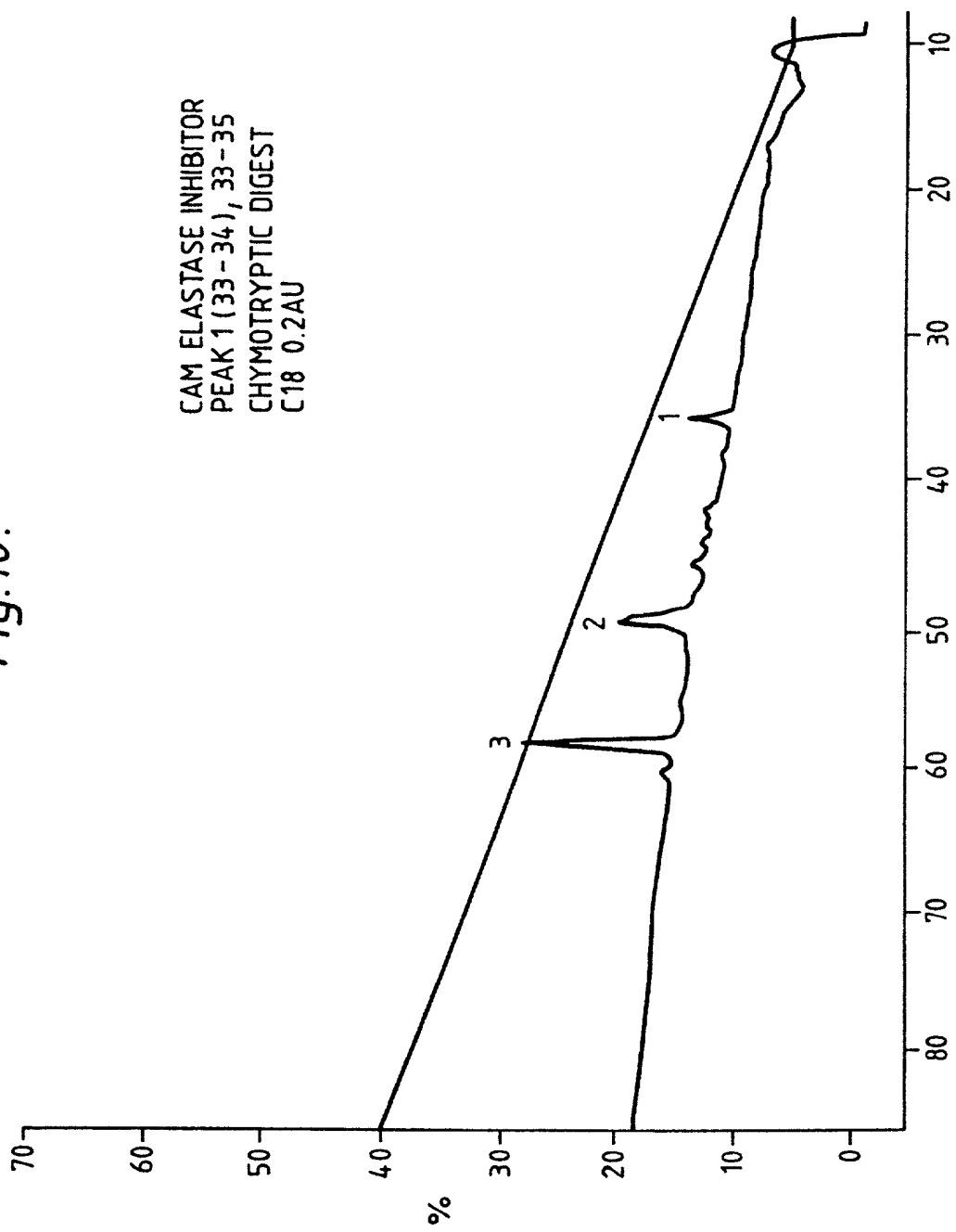
X = UNIDENTIFIED    T = TRYPTIC FRAGMENTS    C = CHYMOTRYPTIC FRAGMENTS

*Fig. 9.*

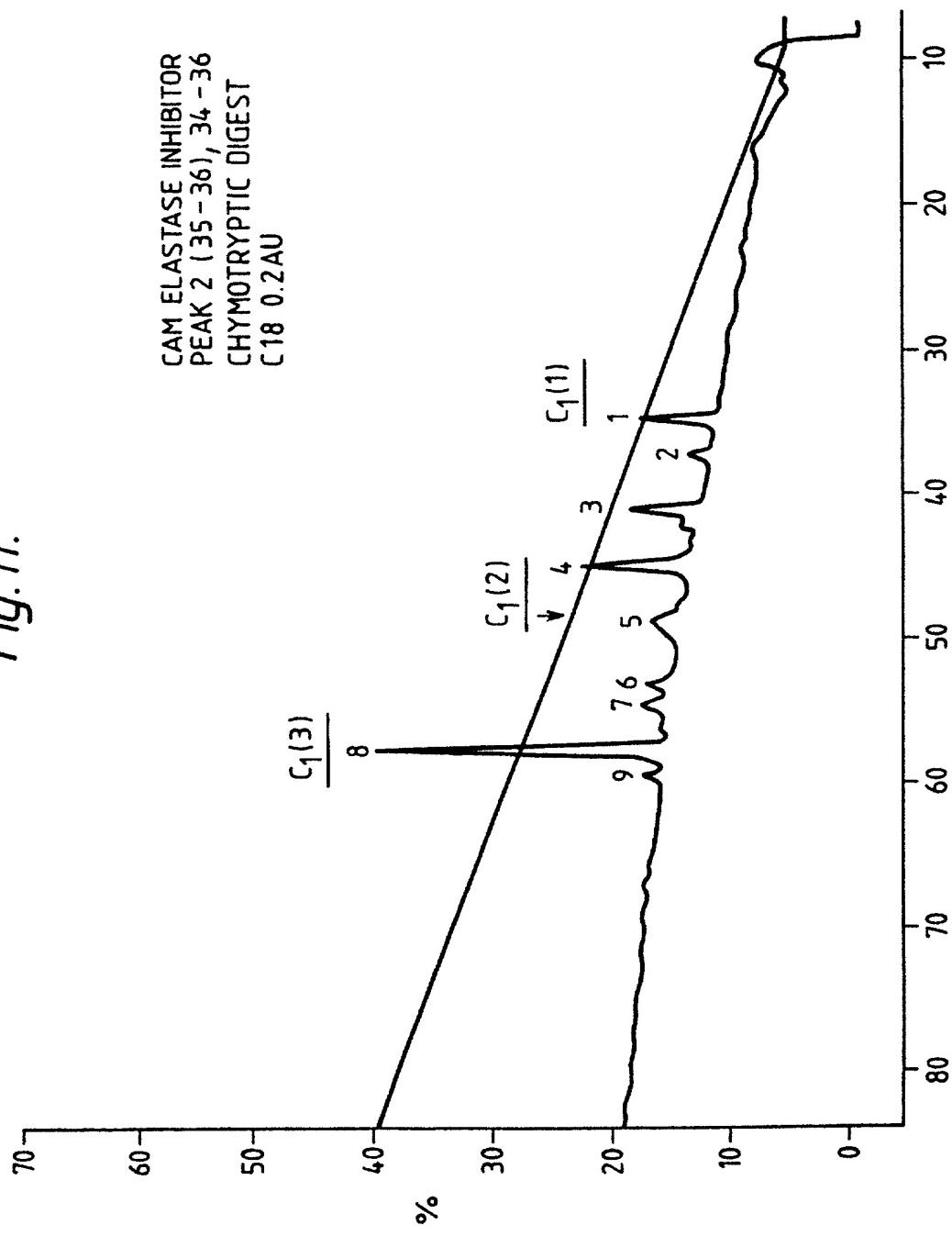


*Fig. 10.*

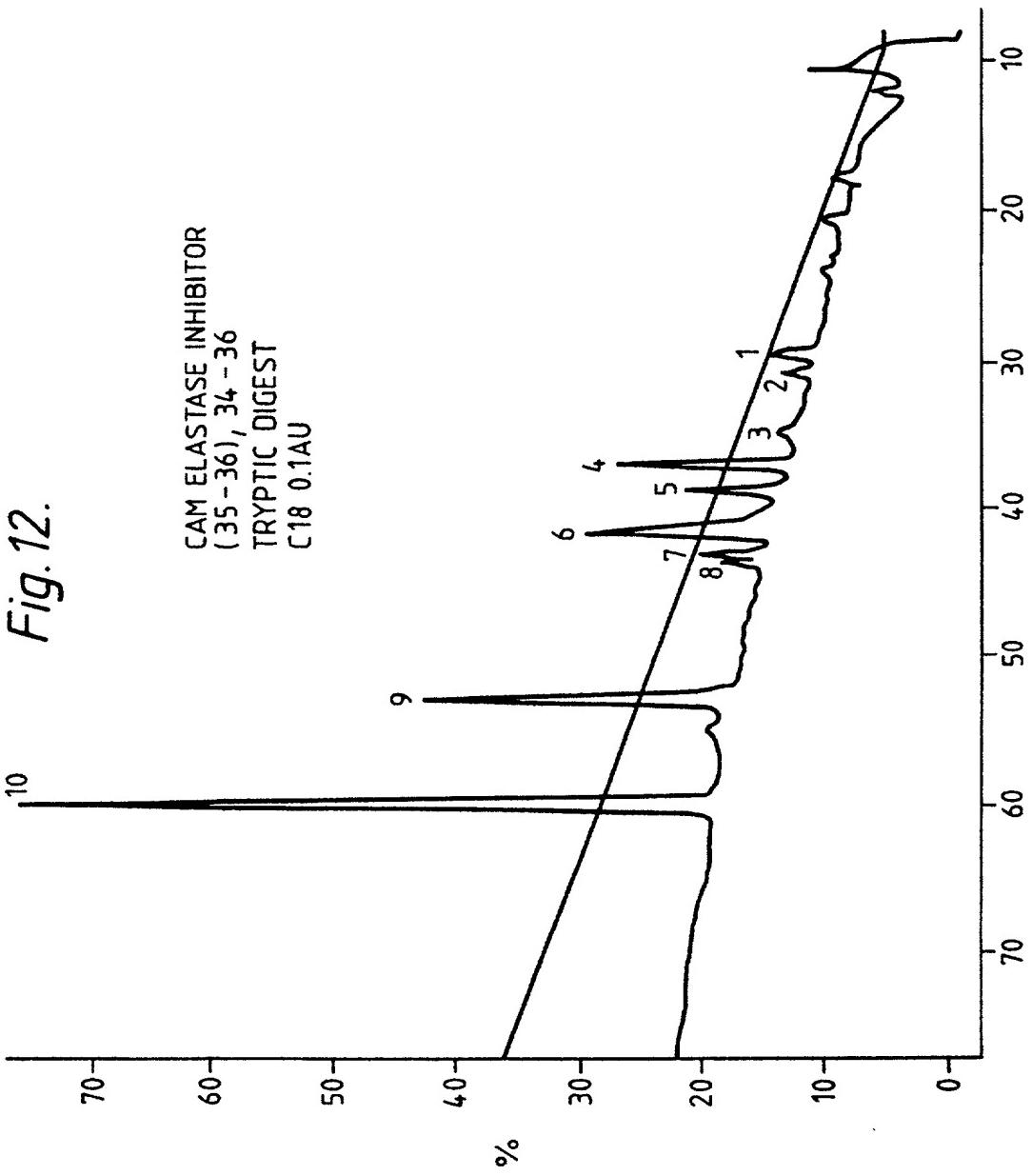
CAM ELASTASE INHIBITOR  
PEAK 1(33 - 34), 33 - 35  
CHYMOTRYPTIC DIGEST  
C18 0.2AU



*Fig. 11.*



*Fig. 12.*



*Fig. 13.*

AlaGlnGluProValLysGlyProValSerThr

1      →      ELI1  
AATT CGAGCTCGGTACCATACCTGCATATGCTCAAGAACCGAGTTAAAGGT CCTGTGTCTACT  
GCTCGAGCCATGGTATGGACGTATCGAGTTCTGGTCAATTCCAGGACACAGATGA

LysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnProProAsnArg

63     →      ELI3  
AAGCCAGGTTCTTGTCCATTATCTTGATT CGTT GCGCTATGTTAAACCCACCTAACCGT  
TTCGGTCCAAGAACAGGATAATAGAAACTAAGCAACGCGATACAATTGGGTGGATTGGCA  
ELI2 ←

CysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySerCysGlyMet

123    →      ELI5  
TGTTTGAAGGACACTGATT GTCCAGGTATCAAAAAGT GCTGTGAAGGTT CCTGCGGTATG  
ACAAA ACTT CCTGTGACTAACAGGTCCATAGTTTCACGACACTTCCAAGGACGCCATAC  
ELI4 ←

AlaCysPheValProGlnEndEnd

183 GCTTGTT CGTT CCACAATAATAG

CGAACAAAGCAAGGTGTTATTATCCTAG 210

ELI6 ←

*Fig. 14.*

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys  
GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC

5' DNA

Sequence

Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys  
CCC ATT ATC TTG ATC CGG TGC GCC ATG TTG AAT CCC CCT AAC CGC TGC

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

TTG AAA GAT ACT GAC TGC CCA GGA ATZ AAG AAP TGC TGT GAA GGC TCT

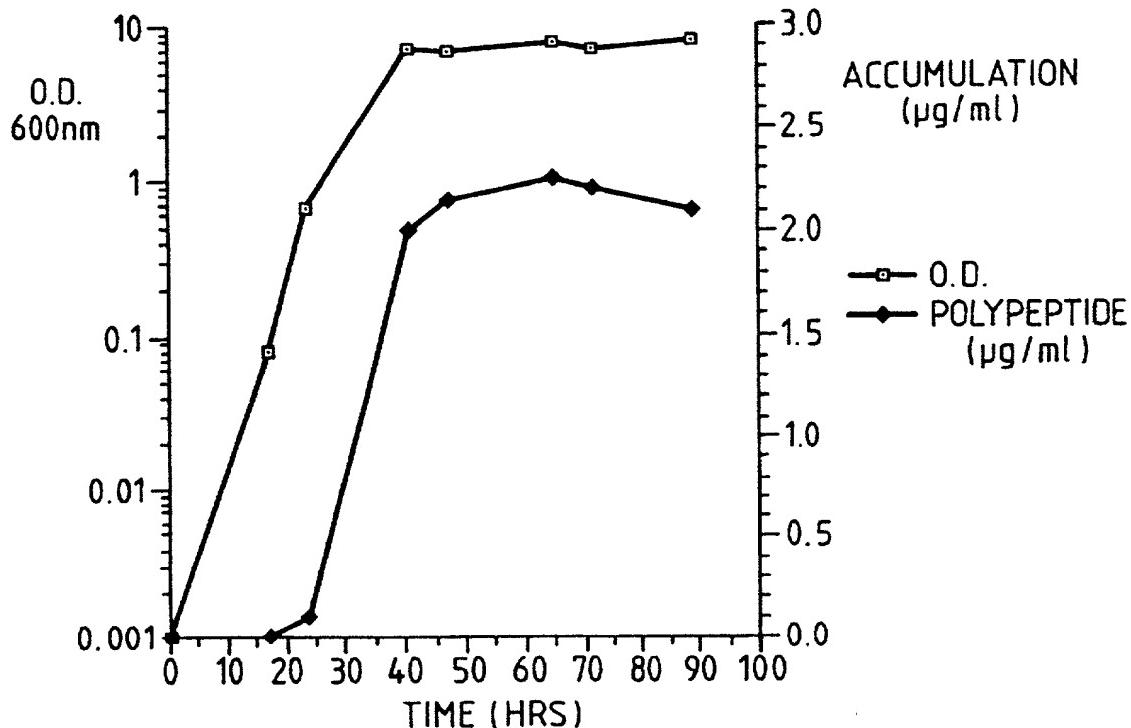
Cys Gly Met Ala Cys Phe Val Pro Gln

TGC GGG ATG GCC TGT TTC GTT CCC CAG

Z = T, C or A

P = A or G

*Fig. 19.*



# *Fig. 15.*

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys  
GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC

5' DNA

Sequence

Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys  
CCC ATT ATC TTG ATC CGG TGC GCC ATG TTG AAT CCC CCT AAC CGC TGC

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

TTG AAA GAT ACT GAC TGC CCA GGA ATZ AAG AAP TGC TGT GAA GGC TCT

Cys Gly Met Ala Cys Phe Val Pro Gln

TGC GGG ATG GCC TGT TTC GTT CCC CAG TAG GAGGGAGCCGGTCCTTGCTGCACCTGT

GCCGTCCCCAGAGCTACAGGGCCCCATCTGGTCCTAAGTCCCTGCTGCCCTTCCCACACTGTCCA  
TTCTTCCTCCCATTCAAGGATGCCAACGGCTGGAGCTGCCTCTCATCCACTTCCAATAAAAGAGTTCCG  
GAATTC

Poly A 3'

signal

Z = T, C or A

P = A or G

*Fig. 16.*

## *Fig. 16 (cont.)*

190

210

230

AGTCTCCACTAACGCCTGGCTCCTGCCCAATTATCTTGATCCGGTGC GCCATGTTGAATCC  
oValSerThrLysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnPr

250

270

290

CCCTAACCGCTGCTTGAAAGATACTGACTGCCAGGAATCAAGAAGTGCTGTGAAGGCTC  
oProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySe

310

330

350

TTGCAGGGATGGCCTGTTGTTCCCCAGTGAGAGGGAGCCGGTCCTGCTGCACCTGTGC  
rCysGlyMetAlaCysPheValProGlnEnd

370

390

410

CGTCCCCAGAGCTACAGGCCCATCTGGTCTTAAGTCCCTGCTGCCCTCCCTCCCAC

430

450

470

ACTGTCCATTCTCCTCCCATTCAAGGATGCCACGGCTGGAGCTGCCTCTCTCATCCACT

490

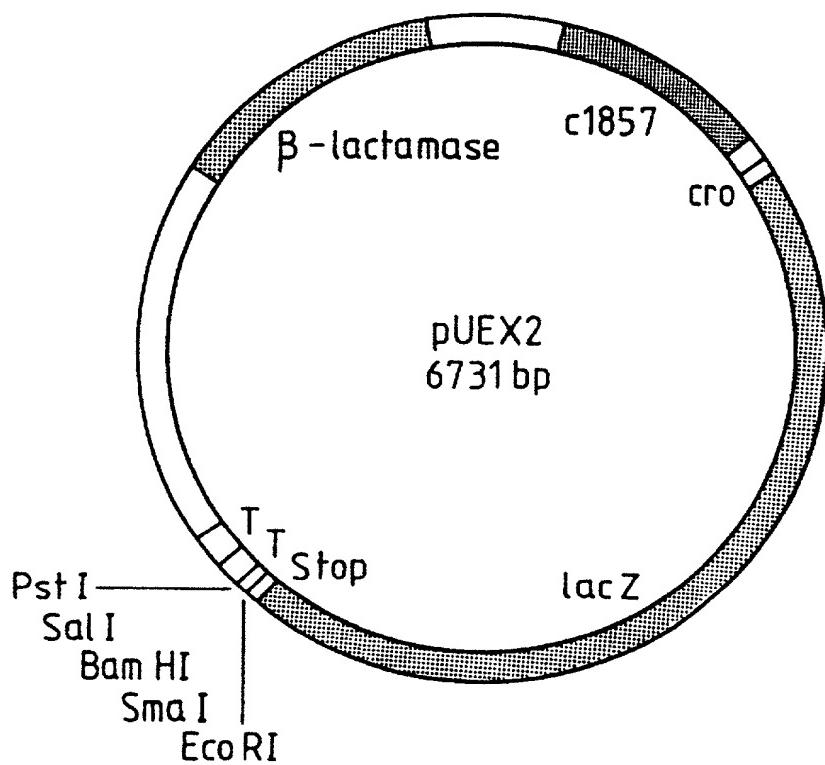
TTCCAATAAGAGTTCCGGAATTC

Poly A

signal

EcoRI

Fig. 17.



pUEX2      EcoRI    SmaI    BamHI    SalI                      PstI  
              |          |          |          |                      |  
              GAA    TTC    CCG    GGG    ATC    CGT    CGA    CCT    GCA    GCC    AAG    CTT    GCT    GAT    TGA  
              Glu    Phe    Pro    Gly    Ile    Arg    Arg    Pro    Ala    Ala    Lys    Leu    Ala    Asp    \*\*\*

*Fig. 18.*

